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================================================================
Sequence Listing could not be accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: Mon Sep 17 15:07:54 EDT 2007
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Reviewer Comments:
<210>  18
<211>  7
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Variant

<400>  18

Thr Leu Ala Gly Thr Asp Asn
1               5

The above <223> response is an insufficient explanation of "<213>
Artificial Sequence;" please explain the source of the genetic material.
 Same error in Sequences 19 and 20.
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Application No: 10562021   Version No: 2.0

Input Set:

Output Set:

Started: 2007-09-10 11:59:07.073
Finished: 2007-09-10 11:59:11.103
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 30 ms
Total Warnings: 9
Total Errors: 0
No. of SeqIDs Defined: 20
Actual SeqID Count: 20

Error code	Error Description
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<110>   Novozymes A/S

<120>   CGTASE VARIANTS

<130>   10340-WO

<140>   10562021
<141>   2006-01-11

<160>   20

<170>   PatentIn version 3.4

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<211>   713
<212>   PRT
<213>   Bacillus agaradherens

<400>   1

Met Ser Lys Lys Thr Leu Lys Arg Leu Leu Ala Leu Val Val Val Leu
1   5   10   15

Phe Ile Leu Ser Gly Ser Gly Ile Leu Asp Phe Ser Ile Thr Ser Ala
            20   25   30

Asn Ala Gln Gln Ala Thr Asp Arg Ser Asn Ser Val Asn Tyr Ser Thr
        35   40   45

Asp Gly Ile Tyr Gln Ile Val Thr Asp Arg Phe Tyr Asp Gly Asp Glu
        50   55   60

Ser Asn Asn Pro Ser Gly Glu Leu Tyr Ser Glu Gly Cys Lys Asn Leu
65   70   75   80

Arg Lys Tyr Cys Gly Gly Asp Trp Gln Gly Ile Ile Asp Lys Ile Asp
                85   90   95

Asp Gly Tyr Leu Thr Asn Met Gly Val Thr Ala Leu Trp Ile Ser Pro
            100   105   110

Pro Val Glu Asn Ile Phe Glu Thr Ile Asp Asp Glu Ser Gly Thr Thr
            115   120   125

Ser Tyr His Gly Tyr Trp Ala Arg Asp Tyr Lys Lys Thr Asn Pro Phe
        130   135   140

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Phe Gly Ser Thr Glu Asp Phe Glu Arg Leu Ile Glu Thr Ala His Ser
145             150             155             160

His Asp Ile Lys Ile Val Ile Asp Leu Ala Pro Asn His Thr Ser Pro
                165             170             175

Ala Asp Phe Asp Asn Pro Asn Tyr Ala Glu Asn Gly Ile Leu Tyr Asp
            180             185             190

Asn Gly Asn Tyr Val Ser Ser Tyr Ser Asp Asn Ser Asp Leu Phe Leu
        195             200             205

Tyr Asn Gly Gly Thr Asp Phe Ser Thr Tyr Glu Asp Glu Ile Tyr Arg
    210             215             220

Asn Leu Phe Asp Leu Ala Ser Phe Asn His Ile Asn Ala Glu Leu Asn
225             230             235             240

Asn Tyr Leu Glu Asp Ala Val Lys Lys Trp Leu Asp Leu Gly Ile Asp
            245             250             255

Gly Ile Arg Ile Asp Ala Val Ala His Met Pro Pro Gly Trp Gln Lys
        260             265             270

Ala Tyr Met Asp Thr Ile Tyr Asp His Arg Ala Val Phe Thr Phe Gly
    275             280             285

Glu Trp Phe Thr Gly Pro Tyr Gly Asn Glu Asp Tyr Thr Lys Phe Ala
    290             295             300

Asn Asn Ser Gly Met Ser Val Leu Asp Phe Arg Phe Ala Gln Thr Thr
305             310             315             320

Arg Asn Val Ile Gly Asn Asn Asn Gly Thr Met Tyr Asp Ile Glu Lys
            325             330             335

Met Leu Thr Asp Thr Glu Asn Asp Tyr Asp Arg Pro Gln Asp Gln Val
        340             345             350

Thr Phe Leu Asp Asn His Asp Met Ser Arg Phe Thr Asn Asp Gly Glu
    355             360             365
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```
Ser Thr Arg Thr Thr Asp Ile Gly Leu Ala Leu Met Leu Thr Ser Arg
    370               375               380

Gly Val Pro Thr Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Glu Gly Asp
385               390               395               400

Gly Asp Pro Gly Ser Arg Gly Met Met Glu Ser Phe Gly Glu Asn Thr
              405               410               415

Asp Ala Tyr Lys Leu Ile Gln Lys Leu Ala Pro Leu Arg Lys Ser Asn
          420               425               430

Pro Ala Tyr Gly Tyr Gly Thr Thr Lys Glu Arg Trp Ile Asn Asp Asp
          435               440               445

Val Ile Ile Tyr Glu Arg Asn Phe Gly Asp Asn Tyr Ala Leu Ile Ala
    450               455               460

Ile Asn Arg Asn Leu Asn Thr Ser Tyr Asn Ile Gln Gly Leu Gln Thr
465               470               475               480

Glu Met Pro Ser Asn Ser Tyr Asp Asp Val Leu Asp Gly Leu Leu Asp
              485               490               495

Gly Gln Ser Ile Val Val Asp Asn Asn Gly Glu Val Asn Glu Phe Gln
              500               505               510

Met Ser Pro Gly Glu Val Gly Val Trp Glu Phe Glu Ala Thr Asn Val
          515               520               525

Asp Lys Pro Ser Ile Gly Gln Val Gly Pro Ile Ile Gly Glu Ala Gly
    530               535               540

Arg Thr Val Thr Ile Ser Gly Glu Gly Phe Gly Ser Ser Pro Gly Thr
545               550               555               560

Val Gln Phe Gly Ser Thr Ser Ala Glu Ile Val Ser Trp Asn Asp Thr
              565               570               575

Val Ile Ile Ile Thr Val Pro Asn Asn Glu Ala Gly Tyr His Asp Ile
          580               585               590

Thr Val Val Thr Glu Asp Glu Gln Val Ser Asn Ala Tyr Glu Phe Glu
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                595                     600                     605


Val Leu Thr Ala Asp Gln Val Thr Val Arg Phe Ile Ile Asp Asn Ala
       610                 615                 620


Glu Thr Lys Met Gly Glu Asn Ile Phe Leu Val Gly Asn Val His Glu
625                     630                 635                 640


Leu Gly Asn Trp Asp Pro Glu Gln Ser Val Gly Arg Phe Phe Asn Gln
               645                 650                 655


Val Val Tyr Gln Tyr Pro Thr Trp Tyr Tyr Asp Val Asn Val Pro Ala
               660                 665                 670


Asn Thr Asp Leu Glu Phe Lys Phe Ile Lys Ile Asp Gln Asp Asn Asn
           675                 680                 685


Val Thr Trp Gln Ser Gly Ala Asn His Thr Tyr Ser Ser Pro Glu Ser
       690                 695                 700


Gly Thr Gly Ile Ile Arg Val Asp Trp
705                 710



<210>   2
<211>   713
<212>   PRT
<213>   Bacillus agaradherens

<400>   2

Met Arg Lys Lys Thr Leu Lys Arg Leu Leu Thr Leu Val Val Gly Leu
1               5                   10                  15


Val Ile Leu Ser Gly Leu Ser Ile Leu Asp Phe Ser Ile Thr Ser Ala
           20                  25                  30


Ser Ala Gln Gln Ala Thr Asp Arg Ser Asn Ser Val Asn Tyr Ser Thr
       35                  40                  45


Asp Val Ile Tyr Gln Ile Val Thr Asp Arg Phe Tyr Asp Gly Asp Glu
   50                  55                  60


Ser Asn Asn Pro Ser Gly Glu Leu Tyr Ser Glu Asp Cys Lys Asn Leu
65                  70                  75                  80
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Arg Lys Tyr Cys Gly Gly Asp Trp Gln Gly Ile Ile Asp Lys Ile Asp
                85   90   95

Asp Gly Tyr Leu Thr Asn Met Gly Val Thr Ala Leu Trp Ile Ser Pro
                100   105   110

Pro Val Glu Asn Ile Phe Glu Thr Ile Asp Asp Glu Phe Gly Thr Thr
        115   120   125

Ser Tyr His Gly Tyr Trp Ala Arg Asp Tyr Lys Lys Thr Asn Pro Phe
        130   135   140

Phe Gly Ser Thr Glu Asp Phe Glu Arg Leu Ile Glu Thr Ala His Ser
145   150   155   160

His Asp Ile Lys Ile Val Ile Asp Leu Ala Pro Asn His Thr Ser Pro
                165   170   175

Ala Asp Phe Asp Asn Pro Asp Tyr Ala Glu Asn Gly Val Leu Tyr Asp
                180   185   190

Asp Gly Asn Tyr Leu Gly Ser Tyr Ser Asp Asp Ser Asp Leu Phe Leu
        195   200   205

Tyr Asn Gly Gly Thr Asp Phe Ser Asn Tyr Glu Asp Glu Ile Tyr Arg
        210   215   220

Asn Leu Phe Asp Leu Ala Ser Phe Asn His Ile Asn Ser Glu Leu Asn
225   230   235   240

Asn Tyr Leu Glu Asp Ala Val Lys Lys Trp Leu Asp Leu Gly Ile Asp
                245   250   255

Gly Ile Arg Ile Asp Ala Val Ala His Met Pro Pro Gly Trp Lys Lys
                260   265   270

Ala Tyr Met Asp Thr Ile Tyr Asp His Arg Ala Val Phe Thr Phe Gly
        275   280   285

Glu Trp Phe Thr Gly Pro Ser Gly Asn Glu Asp Tyr Thr Lys Phe Ala
        290   295   300

Asn Asn Ser Gly Met Ser Val Leu Asp Phe Arg Phe Ala Gln Thr Thr
305   310   315   320

Arg Asn Val Ile Gly Asn Asn Asn Gly Thr Met Tyr Asp Ile Glu Lys
                325   330   335

Met Leu Thr Asp Thr Glu Asn Asp Tyr Asp Arg Pro Gln Asp Gln Val
                340   345   350

Thr Phe Leu Asp Asn His Asp Met Ser Arg Phe Thr Asn Gly Gly Glu
        355   360   365

Ser Thr Arg Thr Thr Asp Ile Gly Leu Ala Leu Met Leu Thr Ser Arg
        370   375   380

Gly Val Pro Thr Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Lys Gly Asp
385   390   395   400

Gly Asp Pro Gly Ser Arg Gly Met Met Ala Ser Phe Asp Glu Asn Thr
                405   410   415

Asp Ala Tyr Lys Leu Ile Gln Lys Leu Ala Pro Leu Arg Lys Ser Asn
                420   425   430

Pro Ala Tyr Gly Tyr Gly Thr Thr Thr Glu Arg Trp Ile Asn Asp Asp
        435   440   445

Val Leu Ile Tyr Glu Arg His Phe Gly Glu Asn Tyr Ala Leu Ile Ala
        450   455   460

Ile Asn Arg Ser Leu Asn Thr Ser Tyr Asn Ile Gln Gly Leu Gln Thr
465   470   475   480

Glu Met Pro Ser Asn Ser Tyr Asp Asp Val Leu Asp Gly Leu Leu Asp
                485   490   495

Gly Gln Ser Ile Val Val Asp Asn Lys Gly Gly Val Asn Glu Phe Gln
                500   505   510

Met Ser Pro Gly Glu Val Ser Val Trp Glu Phe Glu Ala Glu Asn Val
        515   520   525

Asp Lys Pro Ser Ile Gly Gln Val Gly Pro Ile Ile Gly Glu Ala Gly

Arg Thr Val Thr Ile Ser Gly Glu Gly Phe Gly Ser Ser Gln Gly Thr
545   550   555   560

Val His Phe Gly Ser Thr Ser Ala Glu Ile Leu Ser Trp Asn Asp Thr
                        565   570   575

Ile Ile Thr Leu Thr Val Pro Asn Asn Glu Ala Gly Tyr His Asp Ile
                        580   585   590

Thr Val Val Thr Glu Asp Glu Gln Val Ser Asn Ala Tyr Glu Phe Glu
            595   600   605

Val Leu Thr Ala Asp Gln Val Thr Val Arg Phe Ile Ile Asp Asn Ala
            610   615   620

Glu Thr Lys Leu Gly Glu Asn Val Phe Leu Val Gly Asn Val His Glu
625   630   635   640

Leu Gly Asn Trp Asp Pro Glu Gln Ser Val Gly Arg Phe Phe Asn Gln
                        645   650   655

Ile Val Tyr Gln Tyr Pro Thr Trp Tyr Tyr Asp Val Asn Val Pro Ala
                        660   665   670

Asn Thr Asp Leu Glu Phe Lys Phe Ile Lys Ile Asp Gln Asp Asn Asn
            675   680   685

Val Ile Trp Gln Ser Gly Ala Asn Gln Thr Tyr Ser Ser Pro Glu Ser
            690   695   700

Gly Thr Gly Ile Ile Arg Val Asp Trp
705   710

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<211>   714
<212>   PRT
<213>   Panibacillus macerans

<400>   3

Met Lys Ser Arg Tyr Lys Arg Leu Thr Ser Leu Ala Leu Ser Leu Ser
1   5   10   15

Met Ala Leu Gly Ile Ser Leu Pro Ala Trp Ala Ser Pro Asp Thr Ser
              20   25   30

Val Asp Asn Lys Val Asn Phe Ser Thr Asp Val Ile Tyr Gln Ile Val
              35   40   45

Thr Asp Arg Phe Ala Asp Gly Asp Arg Thr Asn Asn Pro Ala Gly Asp
              50   55   60

Ala Phe Ser Gly Asp Arg Ser Asn Leu Lys Leu Tyr Phe Gly Gly Asp
65   70   75   80

Trp Gln Gly Ile Ile Asp Lys Ile Asn Asp Gly Tyr Leu Thr Gly Met
                  85   90   95

Gly Val Thr Ala Leu Trp Ile Ser Gln Pro Val Glu Asn Ile Thr Ser
              100   105   110

Val Ile Lys Tyr Ser Gly Val Asn Asn Thr Ser Tyr His Gly Tyr Trp
              115   120   125

Ala Arg Asp Phe Lys Gln Thr Asn Asp Ala Phe Gly Asp Phe Ala Asp
              130   135   140

Phe Gln Asn Leu Ile Asp Thr Ala His Ala His Asn Ile Lys Val Val
145   150   155   160

Ile Asp Phe Ala Pro Asn His Thr Ser Pro Ala Asp Arg Asp Asn Pro
              165   170   175

Gly Phe Ala Glu Asn Gly Gly Met Tyr Asp Asn Gly Ser Leu Leu Gly
              180   185   190

Ala Tyr Ser Asn Asp Thr Ala Gly Leu Phe His His Asn Gly Gly Thr
              195   200   205

Asp Phe Ser Thr Ile Glu Asp Gly Ile Tyr Lys Asn Leu Tyr Asp Leu
              210   215   220

Ala Asp Ile Asn His Asn Asn Asn Ala Met Asp Ala Tyr Phe Lys Ser
225   230   235   240

Ala Ile Asp Leu Trp Leu Gly Met Gly Val Asp Gly Ile Arg Phe Asp
                    245   250   255

Ala Val Lys His Met Pro Phe Gly Trp Gln Lys Ser Phe Val Ser Ser
                    260   265   270

Ile Tyr Gly Gly Asp His Pro Val Phe Thr Phe Gly Glu Trp Tyr Leu
                    275   280   285

Gly Ala Asp Gln Thr Asp Gly Asp Asn Ile Lys Phe Ala Asn Glu Ser
        290   295   300

Gly Met Asn Leu Leu Asp Phe Glu Tyr Ala Gln Glu Val Arg Glu Val
305   310   315   320

Phe Arg Asp Lys Thr Glu Thr Met Lys Asp Leu Tyr Glu Val Leu Ala
                    325   330   335

Ser Thr Glu Ser Gln Tyr Asp Tyr Ile Asn Asn Met Val Thr Phe Ile
                    340   345   350

Asp Asn His Asp Met Asp Arg Phe Gln Val Ala Gly Ser Gly Thr Arg
                    355   360   365

Ala Thr Glu Gln Ala Leu Ala Leu Thr Leu Thr Ser Arg Gly Val Pro
        370   375   380

Ala Ile Tyr Tyr Gly Thr Glu Gln Tyr Met Thr Gly Asp Gly Asp Pro
385   390   395   400

Asn Asn Arg Ala Met Met Thr Ser Phe Asn Thr Gly Thr Thr Ala Tyr
                    405   410   415

Lys Val Ile Gln Ala Leu Ala Pro Leu Arg Lys Ser Asn Pro Ala Ile
                    420   425   430

Ala Tyr Gly Thr Thr Thr Glu Arg Trp Val Asn Asn Asp Val Leu Ile
        435   440   445

Ile Glu Arg Lys Phe Gly Ser Ser Ala Ala Leu Val Ala Ile Asn Arg
450   455   460

Asn Ser Ser Ala Ala Tyr Pro Ile Ser Gly Leu Leu Ser Ser Leu Pro

Ala Gly Thr Tyr Ser Asp Val Leu Asn Gly Leu Leu Asn Gly Asn Ser
                485   490   495

Ile Thr Val Gly Ser Gly Gly Ala Val Thr Asn Phe Thr Leu Ala Ala
            500   505   510

Gly Gly Thr Ala Val Trp Gln Tyr Thr Ala Pro Glu Thr Ser Pro Ala
        515   520   525

Ile Gly Asn Val Gly Pro Thr Met Gly Gln Pro Gly Asn Ile Val Thr
    530   535   540

Ile Asp Gly Arg Gly Phe Gly Gly Thr Ala Gly Thr Val Tyr Phe Gly
545   550   555   560

Thr Thr Ala Val Thr Gly Ser Gly Ile Val Ser Trp Glu Asp Thr Gln
                565   570   575

Ile Lys Ala Val Ile Pro Lys Val Ala Ala Gly Lys Thr Gly Val Ser
                580   585   590

Val Lys Thr Se